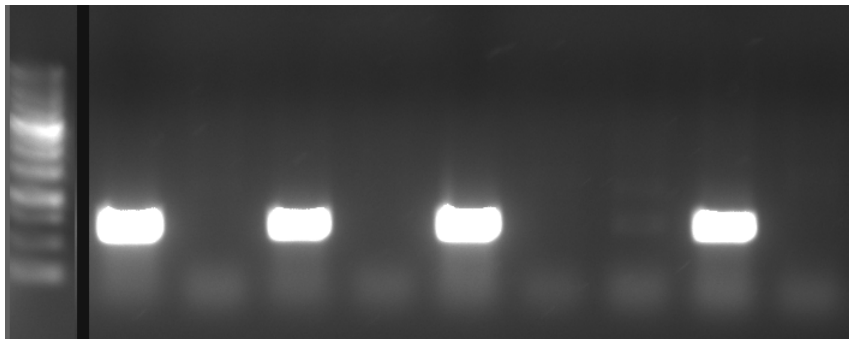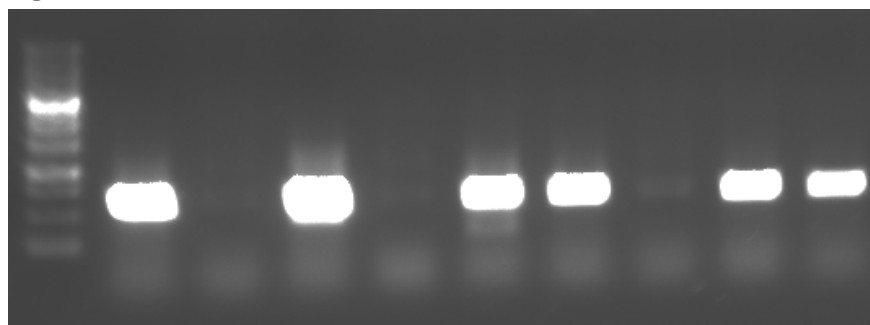**PCR: NTF**

Froglet # 1* 2 3* 4 5* 6 7 8* 9

PCR: BirA

Froglet # 1 2 3 4 5 6 7 8 9

Supplemental Fig. 1. Toe-clip genomic PCR of mlc2::NTF; CMV::BirA juvenile frogs. PCR amplification of genomic DNA obtained from juvenile frogs generated by REMI transgenesis with the co-injection of mlc2p::xNTF and CMV::BirA. Asterisk (*) denotes froglets with GFP expression confirmed by visualization during embryogenesis. All four froglets are also confirmed to harbor DNA corresponding to CMV::BirA transgene. Two additional froglets (#6 and #9) were also positive for the CMV::BirA transgene.
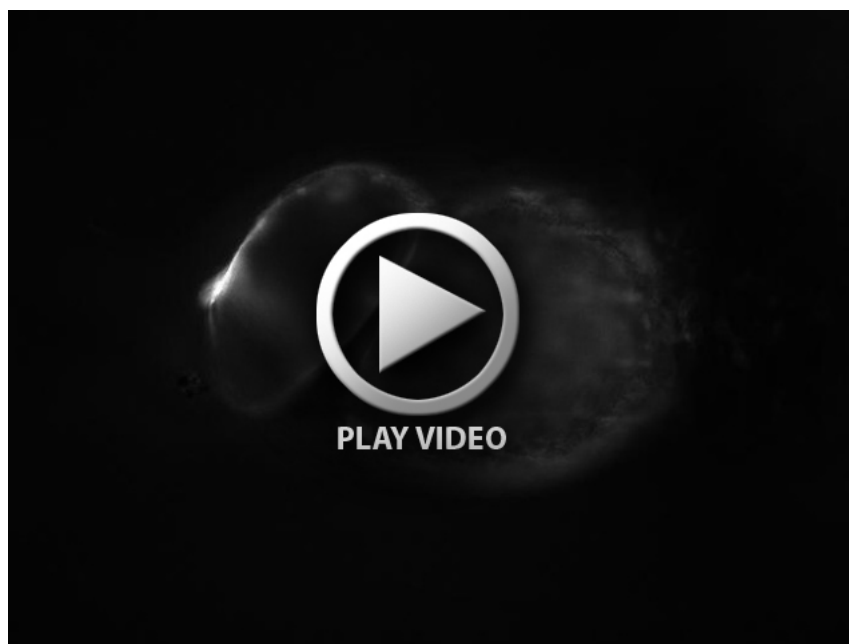
Supplemental Movie 1. Live time-lapse imaging of beating heart in CA::NTF transgenic tadpoles (stage 50).

Supplemental Table 1. Primers used for qRT-PCR.

Download Table S1

Supplemental Table 2. List of protein clusters from proteomic profiling of INTACT-enriched nuclei. Excel spreadsheets of protein clusters assembled by Scaffold and illustrated in Fig. 6A. For each cluster the following are provided: gene symbol (X. tropicalis, if available), UniProt accession, Description (*X. laevis*, if available), number of accession per cluster/group, molecular weight (kDa), weighted spectral counts for each biological replicate (A-C), spectral count percent coefficient of variation, and exclusive (non-shared) peptides for each replicate (A-C), and letter reference code for cluster identification in biological replicates. Protein clusters are listed in different sheets as "Collapsed" and "Expanded" formats.

Download Table S2

Supplemental Table 3. Gene ontology enrichment and classification. (Sheet 1) List of statistically enriched (p-value <0.01) biological processes identified by g:profiler illustrated in Fig. 6B. Ten biological process GO terms are listed with associated p-values, Term ID, # of total annotated X. tropicalis genes in respective term, # of total genes used for input, # of input genes that were annotated to the respective term, and the list of genes within the respective term. (Sheet2) List of genes with annotation to nucleic acid binding molecular function ontology (see Fig. 6C,D). Genes symbols were converted to ENSEMBL Gene ID with G:convert and cross-referenced to Human ENSEMBL ID orthologues using ENSEMBL Biomart. As in supplementary material Table S2, the following are provided: UniProt accessions, weighted spectrum counts for each replicate (A-C), percent coefficient of variation (≥3 spectral counts), and letter replicate reference for cluster identification in biological replicates.

Download Table S3